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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/823,307C

DATE: 09/05/2002

TIME: 08:41:47

PHLS

Input Set : A:\7853235999.txt

Output Set: N:\CRF4\09052002\I823307C.raw

3 <110> APPLICANT: KroczeK, Richard  
5 <120> TITLE OF INVENTION: METHODS OF MODULATING T LYMPHOCYTE COSTIMULATION  
7 <130> FILE REFERENCE: 7853-235-999  
9 <140> CURRENT APPLICATION NUMBER: 09/823,307C  
C--> 10 <141> CURRENT FILING DATE: 2001-04-02  
12-<150> PRIOR APPLICATION NUMBER: 09/509,283  
13 <151> PRIOR FILING DATE: 2000-08-11  
15 <150> PRIOR APPLICATION NUMBER: PCT/DE98/02896  
16 <151> PRIOR FILING DATE: 1998-09-23  
18 <150> PRIOR APPLICATION NUMBER: DE 19821060.4  
19 <151> PRIOR FILING DATE: 1998-05-11  
21 <150> PRIOR APPLICATION NUMBER: DE 19741929  
22 <151> PRIOR FILING DATE: 1997-09-23  
24 <160> NUMBER OF SEQ ID NOS: 5  
26 <170> SOFTWARE: PatentIn version 3.0  
28 <210> SEQ ID NO: 1  
29 <211> LENGTH: 2641  
30 <212> TYPE: DNA  
31-<213> ORGANISM: 8F4  
33 <220> FEATURE:  
34 <221> NAME/KEY: CDS  
35 <222> LOCATION: 68..667  
37 <400> SEQUENCE: 1  
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39 ggcaaac atg aag tca ggc ctc tgg tat ttc ttt ctc ttc tgc ttg cgc 109  
40 Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg  
41 1 5 10  
42 att aaa gtt tta aca gga gaa atc aat ggt tct gcc aat tat gag atg 157  
43 Ile Lys Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met  
44 15 20 25 30  
45 ttt ata ttt cac aac gga ggt gta caa att tta tgc aaa tat cct gac 205  
46 Phe Ile Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp  
47 35 40 45  
48 att gtc cag caa ttt aaa atg cag ttg ctg aaa ggg ggg caa ata ctc 253  
49 Ile Val Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu  
50 50 55 60  
51 tgc gat ctc act aag aca aaa gga agt gga aac aca gtg tcc att aag 301  
52 Cys Asp Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys  
53 65 70 75  
54 agt ctg aaa ttc tgc cat tct cag tta tcc aac aac agt gtc tct ttt 349  
55 Ser Leu Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe  
56 80 85 90  
57 ttt cta tac aac ttg gac cat tct cat gcc aac tat tac ttc tgc aac 397

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58 Phe Leu Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn
59 95 100 105 110
60 cta tca att ttt gat cct cct cct ttt aaa gta act ctt aca gga gga 445
61 Leu Ser Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly
62 115 120 125
63 tat ttg cat att tat gaa tca caa ctt tgt tgc cag ctg aag ttc tgg 493
64 Tyr Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp
65 130 135 140
66 tta ccc ata gga tgt gca gcc ttt gtt gta gtc tgc att ttg gga tgc 541
67 Leu Pro Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys
68 145 150 155
69 ata ctt att tgt tgg ctt aca aaa aag aag tat tca tcc agt gtg cac 589
70 Ile Leu Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His
71 160 165 170
72 gac cct aac ggt gaa tac atg ttc atg aga gca gtg aac aca gcc aaa 637
73 Asp Pro Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys
74 175 180 185 190
75 aaa tct aga ctc aca gat gtg acc cta taa tatggaactc tggcaccag 687
76 Lys Ser Arg Leu Thr Asp Val Thr Leu
77 195
78 gcatgaagca cggttgccag ttttcctcaa cttgaagtgc aagattctct tatttcggg 747
79 accacggaga gtctgactta actacataca tcttctgtct gtgttttggt caatctggaa 807
80 gaatgactgt atcagtcaat ggggatttta acagactgcc ttggtactgc cgagtcctct 867
81 caaaacaaac accctcttgc aaccagcttt ggagaaagcc cagctcctgt gtgtcactg 927
82 ggagtggaaat cctgtctccc acatctgtct ctagcagtgc atcagccagt aaaacaaaca 987
83 catttacaag aaaaatgttt taaagatgcc aggggtactg aatctgcaaa gcaaatgagc 1047
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98 agaggctgaa gtcaccctgg gaatcacagt ggtctacctg cattcataat tccaggatct 1947
99 gtgaagagca catatgtgtc agggcacaat tccctctcat aaaaaccaca cagcctggaa 2007
100 attggccctg gcccttcaag atagccttct ttagaatatg atttggttag aaagattctt 2067
101 aatatgtgg aatatgatta ttcttagctg gaatattttc tctacttctt gtctgcatgc 2127
102 ccaaggcttc tgaagcagcc aatgtcgatg caacaacatt tgtaacttta ggtaaactgg 2187
103 gattatgttg tagtttaaca ttttgtaact gtgtgcttat agtttacaag tgagaccoga 2247
104 tatgtcatta tgcatactta tattatctta agcatgtgta atgctggatg tgtacagtac 2307
105 agtactgaac ttgtaatttg aatctagtat ggtgttctgt tttcagctga cttggacaac 2367
106 ctgactggct ttgcacaggt gttccctgag ttgtttgcag gtttctgtgt gtgggggtggg 2427

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107 gtatggggag gagaaccttc atgggtggccc acctggcctg gttgtccaag ctgtgcctcg 2487
108 acacatcctc atccccagca tgggacacct caagatgaat aataattcac aaaatttctg 2547
109 tgaaatcaaa tccagtttta agaggagcca cttatcaaag agattttaac agtagtaaga 2607
110 aggcaaagaa taaacatttg atattcagca actg 2641

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112 &lt;210&gt; SEQ ID NO: 2

113 &lt;211&gt; LENGTH: 199

114 &lt;212&gt; TYPE: PRT

115 &lt;213&gt; ORGANISM: 8F4

117 &lt;400&gt; SEQUENCE: 2

118 Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys

119 1 5 10 15

121 Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile

122 20 25 30

125 Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val

126 35 40 45

128 Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp

129 50 55 60

131 Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu

132 65 70 75 80

134 Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu

135 85 90 95

137 Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser

138 100 105 110

140 Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu

141 115 120 125

143 His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro

144 130 135 140

146 Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu

147 145 150 155 160

149 Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro

150 165 170 175

152 Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser

153 180 185 190

155 Arg Leu Thr Asp Val Thr Leu

156 195

158 &lt;210&gt; SEQ ID NO: 3

159 &lt;211&gt; LENGTH: 17

160 &lt;212&gt; TYPE: DNA

C--&gt; 161 &lt;213&gt; ORGANISM: Artificial

163 &lt;220&gt; FEATURE:

164 &lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Degenerate oligonucleotide

166 &lt;220&gt; FEATURE:

167 &lt;221&gt; NAME/KEY: misc\_feature

168 &lt;222&gt; LOCATION: 3, 9, 15

169 &lt;223&gt; OTHER INFORMATION: n = a, t, g, or c

171 &lt;400&gt; SEQUENCE: 3

W--&gt; 172 mgnctsaacng aygtnac 17

174 &lt;210&gt; SEQ ID NO: 4

175 &lt;211&gt; LENGTH: 17

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Input Set : A:\7853235999.txt

Output Set: N:\CRF4\09052002\I823307C.raw

176 &lt;212&gt; TYPE: DNA

C--&gt; 177 &lt;213&gt; ORGANISM: Artificial

179 &lt;220&gt; FEATURE:

180 &lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Degenerate oligonucleotide

182 &lt;220&gt; FEATURE:

183 &lt;221&gt; NAME/KEY: misc\_feature

184 &lt;222&gt; LOCATION: 3, 9, 15

185 &lt;223&gt; OTHER INFORMATION: n = a, t, g, or c

187 &lt;400&gt; SEQUENCE: 4

W--&gt; 188 mgnytdacng aygtnac

190 &lt;210&gt; SEQ ID NO: 5

191 &lt;211&gt; LENGTH: 7

192 &lt;212&gt; TYPE: PRT

193 &lt;213&gt; ORGANISM: Homo sapiens

195 &lt;220&gt; FEATURE:

196 &lt;221&gt; NAME/KEY: SITE

197 &lt;222&gt; LOCATION: 1

198 &lt;223&gt; OTHER INFORMATION: Xaa = Unknown amino acid

200 &lt;400&gt; SEQUENCE: 5

W--&gt; 201 Xaa Arg Leu Thr Asp Val Thr

202 1

5

17

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/823,307C

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Input Set : A:\7853235999.txt  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 3,9,15

Seq#:4; N Pos. 3,9,15

Seq#:5; Xaa Pos. 1

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/823,307C

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Input Set : A:\7853235999.txt

Output Set: N:\CRF4\09052002\I823307C.raw

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:161 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3  
L:172 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0  
L:177 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4  
L:188 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0  
L:201 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0